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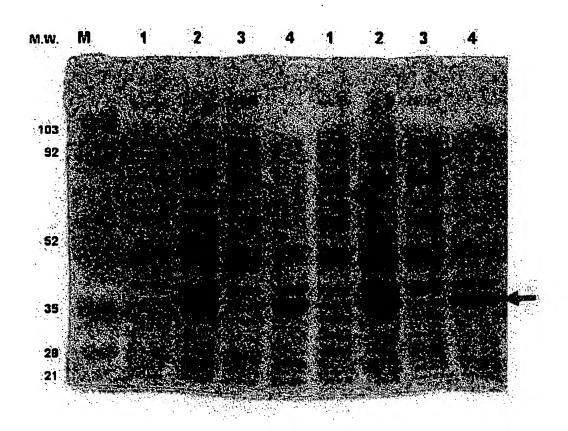
FIG. 1

At5g10410 At2g38230 At3g16050 snz3 snz2 snz1	MEGTGVVAVYGNGAITEAK-KSPFSVKVGLAQMLRGGVIMDVVNAEQARIAEE 52MAGTGVVAVYGEGAMTETKQKSPFSVKVGLAQMLRGGVIMDVVNAEQARIAEE 53 MADQAMTDQDQGAVTLYSGTAITDAKKNHPFSVKVGLAQVLRGGAIVEVSSVNQAKLAES 60MSEFKVKTGLAQMLKGGVIMDVVTPEQAIIAER 33MSEFKVKTGLAQMLKGGVIMDVVTPEQAIIAER 33MTG
At5g10410 At2g38230 At3g16050 snz3 snz2 snz1	AGACAVMALERVPADIRAQGGVARMSDPQMIKEIKQAVTIPVMAKARIGHFVEAQILEAI 112 AGACAVMALERVPADIRAQGGVARMSDPEMIKEIKNAVTIPVMAKARIGHFVEAQILEAI 113 AGACSVIVSDPVRSRGGVRRMPDPVLIKEVKRAVSVPVMARARVGHFVEAQILESL 116 AGACAVMALERIPADMRKSGQVCRMSDPRMIKEIMEAVSIPVMAKVRIGHFVEAQILEEL 93 AGACAVMALERIPADMRKSGQVCRMSDPRMIKEIMEAVSIPVMAKVRIGHFVEAQILEEL 93 SGACAVMALESIPADMRKSGKVCRMSDPKMIKDIMNSVSIPVMAKVRIGHFVEAQIIEAL 95 :***:::::::::::::::::::::::::::::::::
At5g10410 At2g38230 At3g16050 snz3 snz2 snz1	GIDYIDESEVLTLADEDHHINKHNFRIPFVCGCRNLGEALRRIREGAAMIRTKG-EAGTG 171 GVDYVDESEVLTLADEDNHINKHNFKIPFVCGCRNLGEALRRIREGAAMIRTKG-EAGTG 172 AVDYIDESEIISVADDDHFINKHNFRSPFICGCRDTGEALRRIREGAAMIRIQGDLTATG 176 QVDYIDESEVLTPADWTHHIEKHNFKVPFVCGAKDLGEALRRINEGAAMIRTKG-EAGTG 152 QVDYIDESEVLTPADWTHHIEKHNFKVPFVCGAKDLGEALRRINEGAAMIRTKG-EAGTG 152 EVDYIDESEVLTPADWTHHIEKDKFKVPFVCGAKDLGEALRRINEGAAMIRTKG-EAGTG 154 :**:****:::::::::::::::::::::::::::::
At5g10410 At2g38230 At3g16050 snz3 snz2 snz1	NIIEAVRHVRSVNGDIRVLRNMDDDEVFTFAKKLAAPYDLVMQTKQLGRLPVVQFAAG 229 NVVEAVRHVRSVNGAIRLLRSMDDDEVFTYAKKIAAPYDLVVQTKELGRLPVVQFAAG 230 NIAETVKNVRSLMGEVRVLNNMDDDEVFTFAKKISAPYDLVAQTKQMGRVPVVQFASG 234 DVSEAVKHITKIKAEIQQYKENLKTESDFAAKATELRVPVDLLKTTLSEGKLPVVNFAAG 212 DVSEAVKHITKIKAEIQQYKENLKTESDFAAKATELRVPVDLLKTTLSEGKLPVVNFAAG 212 DVSEAVKHIRRITEEIKACQQ-LKSEDDIAKVAEEMRVPVSLLKDVLEKGKLPVVNFAAG 213 :: *:*:: : : : : : : : : : : : : : : :
At5g10410 At2g38230 At3g16050 snz3 snz2 snz1	GVATPADAALMMQLGCDGVFVGSGIFKSGDPARRARAIVQAVTHYSDPEMLVEVSCGLGE 289 GVATPADAALMMQLGCDGVFVGSGVFKSGDPVKRAKAIVQAVTNYRDAAVLAEVSCGLGE 290 GITTPADAALMMQLGCDGVFVGSEVFDGPDPFKKLRSIVQAVQHYNDPHVLAEMSSGLEN 294 GVATPADAALLMQLGCEGVFVGSGIFKSSDPEKLACAIVEATTHYDNPAKLLQVSSDLGD 272 GVATPADAALLMQLGCEGVFVGSGIFKSSDPEKLACAIVEATTHYDNPAKLLQISSDLGD 272 GVATPADAALLMQLGCDGVFVGSGIFKSSNPVRLATAVVEATTHFDNPSKLLEVSSDLGE 273 *::**********************************
At5g10410 At2g38230 At3g16050 sn23 sn22 snz1	AMVGINLNDEKVERFANRSE 309 AMVGLNLDD-KVERFASRSE 309 AMESLNVRGDRIQDFGQGSV 314 LMGGISIQSINEAGGKNGARLSEIGW 298 LMGGISIQSINEAGGKNGARLSEIGW 298 LMGGVSIESISHASNGVRLSEIGW 297 * .:.: .

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FIG. 2



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FIG. 3A

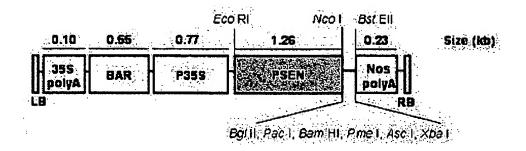


FIG. 3B



FIG. 4

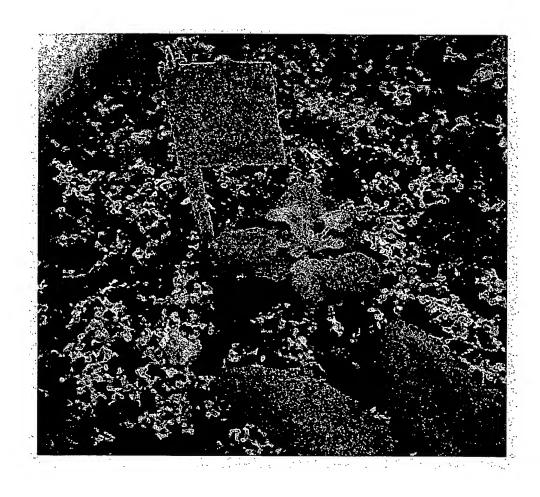


FIG. 5A

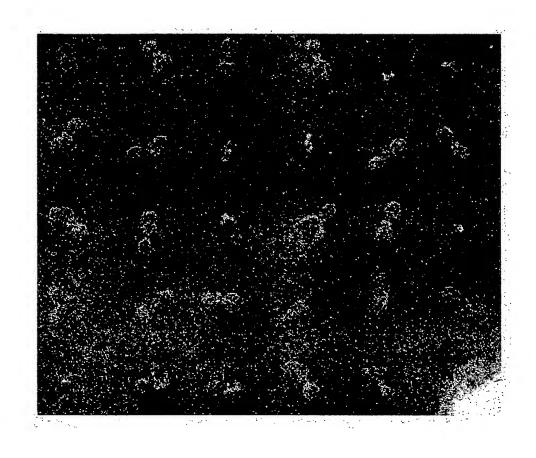
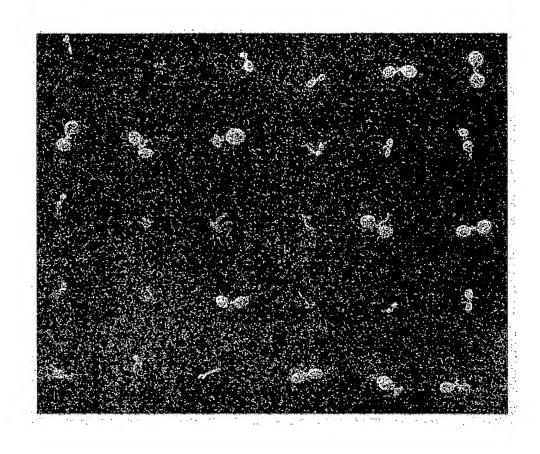


FIG. 5B



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FIG. 5C

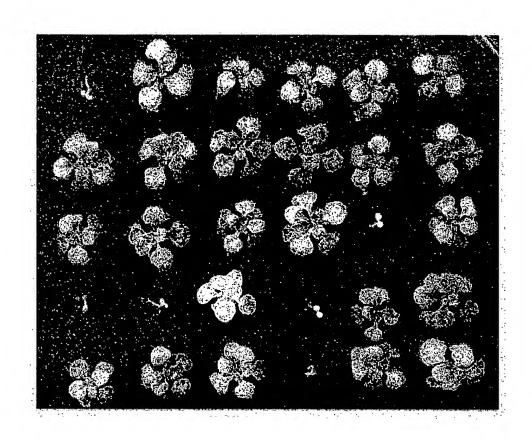
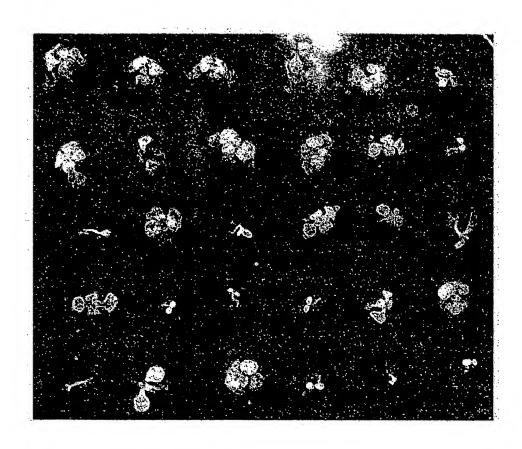


FIG. 5D



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FIG. 6A

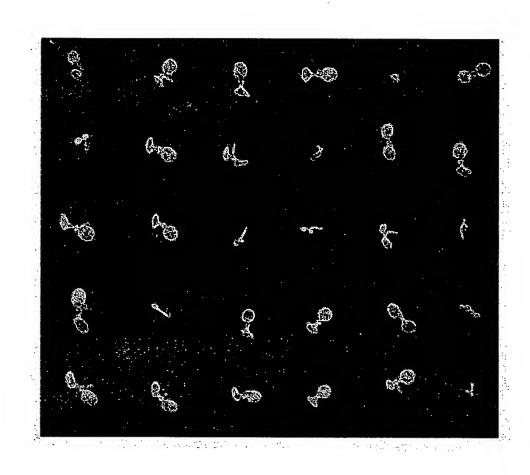
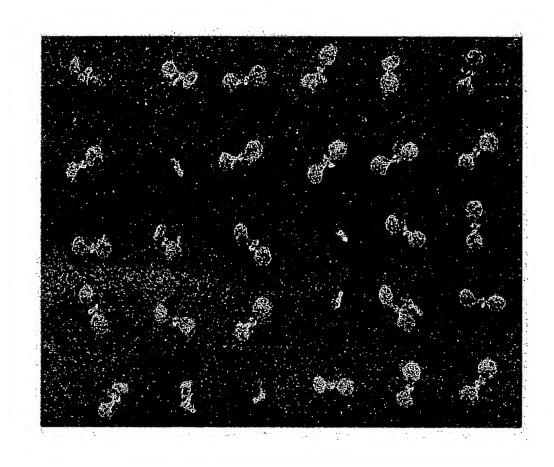
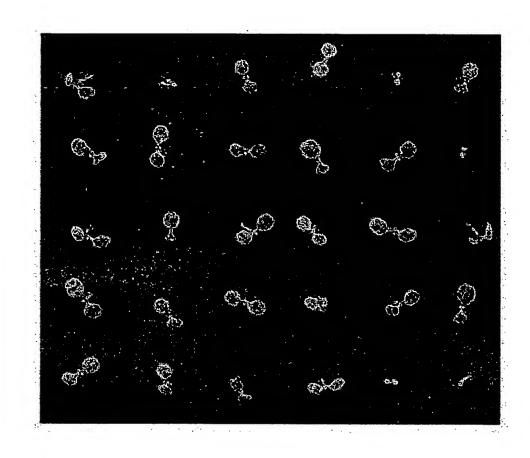


FIG. 6B



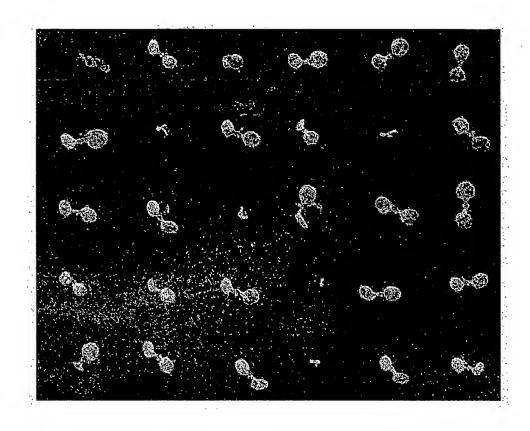
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FIG. 6C



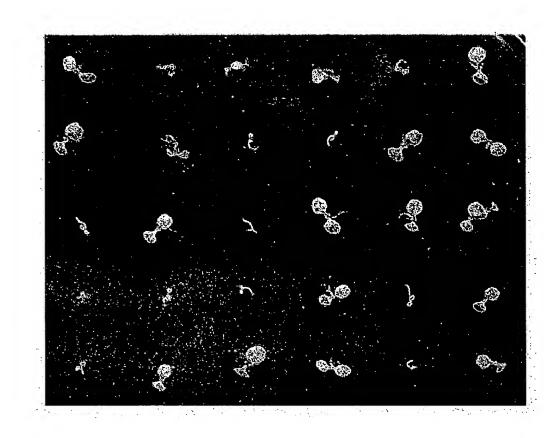
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FIG. 6D



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FIG. 6E



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